SEQUENCE LISTING Thomas Buehler, Reto Andreas Gadient, Reinhard Korn, Rao Movva pCAR and its uses <130> 4-31499A <160> <170> PatentIn version 3.0 <210> <211> 4286 DNA <213> porcine <220> <221> CDS <222> (3229)..(4014)<400> 1 cggtgcgggc ctcttcgcta btacgccagc tggcgaaagg gggatgtgct gcaaggcgat 60 taagttgggt aacgccaggg ttttcccagt cacgacgttg taaaacgacg gccagtgcca 120 agttgggatc tttgcattgg cccacggctc tcaggatggg gatgctcccc ttcagcaccc 180 ggttcccctt ggaaactgat ggtcctgg&t ctgtggcatg gcagtggcac tgtgaggagc 240 ccctaccage ageacacagt gggtttggca etgccacget ccggatgccg cgctctgatc 300 caaccccata atcaagggaa cccgaattgc cc2attatg cccccaccac ccccatcctg 360 ccgggccctc acaccccacg ctgccttgtg gtgacattcc ccagcccaaa cccacggctt 420 catggctacc gcggggcatt tcccattgcc gccccattat cagctctgca cacctcccgc 480 tgtacccatg cctcgtggct gcccttcttt gacgtataat \cttctaatta atacccggcc 540 ttgtcaaagt ggagcacaaa cgttaattaa ttccccagca ggcaggtaat taacagtgtg 600 actccctttt tgctgcgagt ggggctgata cagagagatg tggcactatg gagcccacgg 660 ggtcctggca ctgggtgccc acggaggtcc ccatgtgctg cagtgtcacc gcctccgagg 720 tgacagtatt gtccctgcgg tgtccctgca gctcagctct gtccacaggg/ccacctccag 780 tttggagggg acacaatgca gccccgatgc aacccatcct cgcagcatcc càgggacaaa 840 gaccccactg caagaccgca cacagggctg ggtcccgctc ccctaatatc tacagtgctt 900 ttgcatggcc ccttaatcaa tgcagttaat cagcatgcgc tcatgcaccg ctctggagct 960

geaaageeee tegeageget geteaceaae acegegeaee geeeeggeee ageetgeage

acgcgctgca aacaggaaag aaacaaaata ttgcccaaat gtaggcaaag gcattcggct

1020

				,	•	
gccttgacct	ccgccgggcc gggcc	ctacc taactcaact	cottactcac	cactcactto	1140	
	ctgccaccgc cgcag				1200	
	cccagcagtg cacto				1260	
	cattagcatt gaact				1320	
	tgdagcgcgc gttgc				1380	
	cagcaccagg cccgt				1440	
	cttagtggtg cagcg				1500	
	acccctcggt gttat				1560	
	catgcactca cactg		•		1620	
	ctcagtggct gcacg				1680	
	cgctgcagct cagts				1740	
	gctccccggg aggtg	\			1800	
ggggagggct	gcacacgcgg acccc	gctec ccctccccaa	a caaagcactg	tggaatcaaa	1860	
aaggggggag	gggggatgga ggggd	gcgtc\acacccccgc	cccacaccct	cacctcgagg	1920	
tgagccccac	gttctgcttc actct	cccca tetcccccc	ctccccaccc	ccaattttgt	1980	
atttatttat	tttttaatta ttttg	tgcag cgabggggg	: aaaaaaaaaaa	ggggcgcgcg	2040	
ccaggcgggg	cggggcgggg cgagg	aacaa aacaaaaca	ı ggcggagagg	tgcggcggca	2100	
gccaatcaga	gcggcgcgct ccgaa	agttt ccttttatg	cgaggcggcg	geggeggegg	2160	
ccctataaaa	agcgaagcgc gcggc	gggcg ggagtcgctg	dettgccttc	gccccgtgcc	2220	
ccgctccgcg	ccgcctcgcg ccgcc	cgccc cggctctgac	tgaccgcgtt	actcccacag	2280	
gtgagcgggc	gggacggccc ttctc	ctccg ggctgtaatt	agcgcttggt	ttaatgacgg	2340	
ctcgtttctt	ttctgtggct gcgtg	aaagc cttaaagggc	tccgggaggg	ccctttgtgc	2400	
ggggggagc	ggctcggggg gtgcg	tgcgt gtgtgtgtg	gtggggagcg	ccgcgtgcgg	2460	
cccgcgctgc	ccggcggctg tgagc	getge gggegeggeg	gegggetttg	tgcgctccgc	2520 ·	
gtgtgcgcga	ggggagcgcg gccgg	gggcg gtgccccgcg	a pacadadada	gctgcgaggg	2580	
gaacaaaggc	tgcgtgcggg gtgtg	tgcgt gggggggtga	gcagggggtg	tgggcgcggc	2640	
ggtcgggctg	taacccccc ctgca	ccccc ctccccgagt	tgctgagcac	ggcccggctt	2700	
cgggtgcggg	gctccgtgcg gggcg	tggcg cggggctcgc	: cgtgccgggc	ggggggtggc	2760	
ggcaggtggg	ggtgccgggc ggggc	ggggc cgcctcgggc	cggggagggc	tcgggggagg	2820	
: .						

,		.		
aacacaac	gg ccccggagcg ccggc	ggctg tcgaggcgcg gcg	gageegea geeattgeet	2880
tttatggt	aa tegtgegaga gggeg	caggg acttcctttg to	ccaaatct ggcggagccg	2940
aaatctgg	ga ggcgccgccg cacco	cctct agcgggcgcg gg	cgaagcgg tgcggcgccg	3000
gcaggaag	ga aatgggcggg gaggg	ectte gtgegtegee ge	geegeegt eccettetee	3060
atctccag	cc cggggctgc cgcag	gggga cggctgcctt cg	gggggac ggggcagggc	3120
ggggttcg	gc ttctggcgtg tgacc	ggcgg ggtttatatc tto	ceettete tgtteeteeg	3180
cageeeee	aa gcttaaggtg cacgg	cccac gtggggacta gtg	gccacc atg gcg ctc Met Ala Leu 1	3237
cta cta	tac ttc ata che etc	tgc gga gtc gcg ga	_	3285
Leu Leu 5	Cys Phe Val Leu Leu 10	Cys Gly Val Ala Asp	Leu Thr Arg Ser	,
ttg agt Leu Ser 20	atc act act cct gad Ile Thr Thr Pro Glu 25	cag atg att gaa aag Gln Met Ile Glu Lys 30	g gcc aaa ggg gaa s Ala Lys Gly Glu 35	3333
		ttt acc ctg ggt cca Phe Thr Leu Gly Pro		3381
		ctg tca cca gct gas Leu Ser Pro Ala Asp		3429
		tct gga gac aaa att Ser Gly Asp Lys Ile 75		3477
		gta cat ttt aca agg Val His Phe Thr Seg 95		3525
		gta aca aat cta cag Val Thr Asn Leu Glr 110		3573
		aaa aag gct cct ggt Lys Lys Ala Pro Gly 125		3621
		ctt aag cct tca ggt Leu Lys Pro Ser Gly 140		3669
Val Asp		gga aat gac ttt aas Gly Asn Asp Phe Lys 155		3717
	•			
			,	

			ggt Gly													3765	
aat Asn 180																3813	
gtt Val																3861	
tgt Cys																3909	
gat Asp	gtg Val	gtt Val 230	cct Pro	cct Pro	tca Ser	aat Asn	aga Arg 235	gct Ala	gga Gly	aca Thr	att Ile	gca Ala 240	gga Gly	gct Ala	gtt Val	3957	
ata (4005	
tgt Cys 260		taa	tcta	agata	aag t	aato	gatca	at aa	atcag	gccat	ato	cacat	ctg			4054	
taga	ggtt	tt a	actt	gcttt	a aa	aaac	cte	cac	cacct	ccc	ccts	gaaco	etg a	aaca	ataaaa	4114	
tgaa	tgca	aat t	gttg	gttgt	t aa	ctte	gttta	tte	gcago	ctta	taat	ggtt	ac a	aaata	aagca	4174	
atag	cato	cac a	aaatt	tcac	ca aa	taaa	ıgcat	tti	tttc	cact	gcat	tcta	agt t	gtgg	gtttgt	4234	
ccaa	acto	cat o	caato	gtato	ct ta	ıtcat	gtct	gga	atce	cgg	gtad	cgag	gct d	g		4286	
<210 <211 <212 <213	> 2 > E	2 261 PRT Dorci	ine							\		\					
<400	> 2	2													•		
Met 1	Ala	Leu	Leu	Leu 5	Cys	Phe	Val	Leu	Leu 10	Cys	Gly	Val	Ala	Asp 15	Leu		
Thr i	Arg	Ser	Leu 20	Ser	Ile	Thr	Thr	Pro 25	Glu	Gln	Met	Ile	Glu 30	Lys	Ala		
															`		

Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn

Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu

40

Glo Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr 65 70 75 80

Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn 85 90 95

Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu 105 110

Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val

Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr 130 135 140

Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu 145 150 155 160

Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
165 170 175

Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met 180 185 190

Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
195 200 205

Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu 210 215 220

Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala 225 230 235 240

Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile 245 250 255

Ile Phe Cys Cys Arg 260

```
<210>
        3
 <211>
        1098
 <212>
        DNA
 <213
        porcine
 <220>
 <221>
        CDS
 <222>
        (1)..(1098)
. <400>
 atg gcg ctc ctg ctg tgc ttc gtg ctc ctg tgc gga gtc gcg gat ctc
                                                                        48
 Met Ala Leu Leu Cys Phe Val Leu Cys Gly Val Ala Asp Leu
 acc aga agt trg agt atc act act cct gaa cag atg att gaa aag gcc
                                                                        96
 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
 aaa ggg gaa act gèç tat ttg cca tgc aga ttt acc ctg ggt cca gaa
                                                                       144
 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
 gac cag ggg ccg ctg gàc atc gag tgg ctg ctg tca cca gct gat aat
                                                                       192
 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
 cag aag gtg gat caa gtg att att tta tat tct gga gac aaa att tat
 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
                     70
 gac gac tac tac caa gat ctg aa gga cga gta cat ttt aca agt aat
                                                                       288
 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
                 85
 gat ctc aaa tca ggt gat gca tca àta aat gta aca aat cta cag ttg
                                                                       336
 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
             100
                                 105
 tca gat att ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt
                                                                       384
 Ser Asp Ile Gly Thr Tyr Gln Cys Lys Vàl Lys Lys Ala Pro Gly Val
                             120
 gga aat aag aag att cag ctg aca gtt ctt ctt aag cct tca ggt aca
                                                                       432
Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Lèu Lys Pro Ser Gly Thr
 aga tgt tat gtt gat gga tca gaa gaa att gga àat gac ttt aaa cta
                                                                       480
 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
 145
                     .150
                                         155
 aaa tgt gaa cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag
                                                                       528
Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
                 165
                                     170
                                                          175
 aaa ttg tcc aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg
                                                                       576
Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
             180
                                 185
```

					tct Ser											624
aca Thr	tac Tyr 210	agc Ser	tgt Cys	acc Thr	gtg Val	aaa Lys 215	aac Asn	aga Arg	gtg Val	ggc Gly	tct Ser 220	gat Asp	cag Gln	tgc Cys	ctg Leu	672
					gtt Val 230										gca Ala 240	720
					gtt Val											768
					aaa Lys											816
					agg Arg											864
					tac Tyr											912
					atg Met 310											960
					ttt Phe											1008
ctc Leu	gct Ala	Lys	gta Val 340	Ala	gcc Ala	Pro	Asn	ctc Leu 345	Ser	cgg Arg	atg Met	gga Gly	gcg Ala 350	gtg Val	cct Pro	1056
					cag Gln			Asp					taa	\		1098
<210		ŀ			,									\		
<213 <213	2> I	865 PRT	i									•			1	
<213	5> F	orci	ne													

<400> 4

Met Ala Leu Leu Cys Phe Val Leu Cys Gly Val Ala Asp Leu 1 5 10 10 15

*

-

Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala 20 25 30

Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
35 40 45

Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn 50 55 60

Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr 65 70 75 80

Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn 85, 90 95

Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
100 105 110

Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val 115 120 125

Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr 130 135 140

Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu 145 150 155 160

Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln 165 170 175

Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met 180 185 190

Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
195 200 205

Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Ġln Cys Leu 210 215 220

Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala 225 230 235 240

Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile

Val Phe Cys Cys His Lys Lys Arg Glu Glu Lys Tyr Glu Lys Glu 260 265 270

Val His His Asp\Ile Arg Glu Asp Val Pro Pro Pro Lys Ser Arg Thr

Ser Thr Ala Arg Ser Tyr Leu Gly Ser Asn His Ser Ser Leu Gly Ser

Met Ser Pro Ser Asn Met, Glu Gly Tyr Ser Lys Thr Gln Tyr Asn Gln

Val Pro Ser Glu Asp Phe Glù Arg Ala Pro Gln Ser Pro Thr Leu Pro

Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro

Val Met Ile Pro Ala Gln Ser Lys Asp\Gly Ser Ile Val